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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/702,718DATE: 08/18/98  
TIME: 13:46:24

INPUT SET: S28089.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Muller-Rober, Bernd  
6 Land-Schutze, Volker  
7 La Cognata, Ursula  
8  
9 (ii) TITLE OF INVENTION: PROCESSES FOR INHIBITING AND FOR  
10 INDUCING FLOWER FORMATION IN PLANTS  
11  
12 (iii) NUMBER OF SEQUENCES: 14  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: FISH & NEAVE  
16 (B) STREET: 1251 Avenue of the Americas  
17 (C) CITY: New York  
18 (D) STATE: New York  
19 (E) COUNTRY: USA  
20 (F) ZIP: 10020  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: US 08/702,718  
30 (B) FILING DATE: 19-MAR-1997  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: DE P4408629.6  
34 (B) FILING DATE: 09-MAR-1994  
35  
36 (viii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: DE P4435366.9  
38 (B) FILING DATE: 22-SEP-1994  
39  
40 (vii) PRIOR APPLICATION DATA:  
41 (A) APPLICATION NUMBER: DE P4438821.7  
42 (B) FILING DATE: 19-OCT-1994  
43  
44 (viii) ATTORNEY/AGENT INFORMATION:  
45 (A) NAME: Haley Jr., James F.  
46 (B) REGISTRATION NUMBER: 27,794

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47 (C) REFERENCE/DOCKET NUMBER: AGREVO-1  
48  
49 (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: 212-596-9000  
51 (B) TELEFAX: 212-596-9090  
52  
53  
54 (2) INFORMATION FOR SEQ ID NO:1:  
55  
56 (i) SEQUENCE CHARACTERISTICS:  
57 (A) LENGTH: 1891 base pairs  
58 (B) TYPE: nucleic acid  
59 (C) STRANDEDNESS: unknown  
60 (D) TOPOLOGY: linear  
61  
62 (ii) MOLECULE TYPE: cDNA to mRNA  
63  
64 (iii) HYPOTHETICAL: NO  
65  
66 (iv) ANTI-SENSE: NO  
67  
68 (vi) ORIGINAL SOURCE:  
69 (A) ORGANISM: Solanum tuberosum  
70 (B) STRAIN: c.v. Desiree  
71 (F) TISSUE TYPE: leaf  
72  
73 (vii) IMMEDIATE SOURCE:  
74 (A) LIBRARY: cDNA library in pBluescriptKS  
75 (B) CLONE: pCBS  
76  
77 (ix) FEATURE:  
78 (A) NAME/KEY: CDS  
79 (B) LOCATION: 73..1485  
80 (D) OTHER INFORMATION: /EC\_number= 4.1.3.7.  
81 /product= "Citrate synthase"  
82  
83  
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
85  
86 TTTTCGTTTC CATCAGCCTA CTTGAGATGT ATTCCCACTG GTAAAAGTTA ATTTTTTTGA 60  
87  
88 TTTTCGCGAG CA ATG GTG TTC TAC CGT AGC GTT TCG TTG CTG TCA AAG 108  
89 Met Val Phe Tyr Arg Ser Val Ser Leu Leu Ser Lys  
90 1 5 10  
91  
92 CTC CGC TCT CGA GCG GTC CAA CAG TCA AAT GTT AGC AAT TCT GTG CGC 156  
93 Leu Arg Ser Arg Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg  
94 15 20 25  
95  
96 TGG CTT CAA GTC CAA ACC TCT TCC GGT CTT GAT CTG CGT TCT GAG CTG 204  
97 Trp Leu Gln Val Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu  
98 30 35 40  
99

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100	GTA CAA GAA TTG ATT CCT GAA CAA CAG GAT CGC CTG AAA AAG ATC AAG	252
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104	TCA GAT ATG AAA GGT TCA ATT GGG AAC ATC ACA GTT GAT ATG GTT CTT	300
105	Ser Asp Met Lys Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu	
106	65 70	75
107		
108	GGT GGA ATG AGA GGA ATG ACA GGA TTA CTG TGG AAA CCT CAT TAC CTT	348
109	Gly Gly Met Arg Gly Met Thr Gly Leu Leu Trp Lys Pro His Tyr Leu	
110	80 85	90
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112	GAC CCT GAT GAG GGA ATT CGC TTC CGG GGG TTG TCT ATA CCT GAA TGC	396
113	Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys	
114	95 100	105
115		
116	CAA AAG GTA TTA CCT GCA GCA AAG CCT GGG GGT GAG CCC TTG CCT GAA	444
117	Gln Lys Val Leu Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu	
118	110 115	120
119		
120	GGT CTT CTC TGG CTT CTT TTA ACA GGA AAG GTG CCA TCA AAA GAG CAA	492
121	Gly Leu Leu Trp Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln	
122	125 130	135 140
123		
124	GTG AAT TCA ATT GTC TCA GGA ATT GCA GAG TCG GGC ATC ATA TCC CTG	540
125	Val Asn Ser Ile Val Ser Gly Ile Ala Glu Ser Gly Ile Ile Ser Leu	
126	145 150	155
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128	ATC ATC ATG TAT ACA ACT ATT GAT GCC TTA CCA GTC ACA GCT CAT CCA	588
129	Ile Ile Met Tyr Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro	
130	160 165	170
131		
132	ATG ACC CAG TTT GCT ACT GGA GTC ATG GCT CTT CAG GTT CAA AGT GAA	636
133	Met Thr Gln Phe Ala Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu	
134	175 180	185
135		
136	TTT CAA AAG GCA TAC GAG AAA GGG ATT CAC AAA TCA AAG TAT TGG GAA	684
137	Phe Gln Lys Ala Tyr Glu Lys Gly Ile His Lys Ser Lys Tyr Trp Glu	
138	190 195	200
139		
140	CCA ACA TAT GAG GAT TCC ATG AAT CTG ATT GCT CAA GTT CCA CTT GTT	732
141	Pro Thr Tyr Glu Asp Ser Met Asn Leu Ile Ala Gln Val Pro Leu Val	
142	205 210	215 220
143		
144	GCT GCT TAT GTT TAT CGC AGG ATG TAC AAG AAT GGT GAC ACT ATA CCT	780
145	Ala Ala Tyr Val Tyr Arg Arg Met Tyr Lys Asn Gly Asp Thr Ile Pro	
146	225 230	235
147		
148	AAG GAT GAA TCC CTG GAT TAT GGT GCA AAT TTT GCT CAC ATG CTT GGT	828
149	Lys Asp Glu Ser Leu Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly	
150	240 245	250
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152	TTC AGT AGC TCT GAA ATG CAT GAA CTT CTT ATG AGG CTC TAT GTA ACA	876

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157	Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala His Thr Gly His	
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159		280
160	TTG GTT GCT AGT GCT TTG TCT GAT CCT TAC CTC TCC TTT GCT GCT GCT	972
161	Leu Val Ala Ser Ala Leu Ser Asp Pro Tyr Leu Ser Phe Ala Ala Ala	
162	285	290
163		295
164	295	300
165	TTG AAT GGT TTA GCC GGA CCA CTT CAT GGT TTA GCC AAT CAG GAA GTT	1020
166	Leu Asn Gly Leu Ala Gly Pro Leu His Gly Leu Ala Asn Gln Glu Val	
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168	310	315
169	TTG CTA TGG ATA AAA TCT GTT GTA GAA GAA TGT GGG GAG AAC ATT TCC	1068
170	Leu Leu Trp Ile Lys Ser Val Val Glu Glu Cys Gly Glu Asn Ile Ser	
171	320	325
172	325	330
173	AAA GAG CAG TTG AAA GAC TAT GTT TGG AAA ACA TTG AAC AGT GGC AAG	1116
174	Lys Glu Gln Leu Lys Asp Tyr Val Trp Lys Thr Leu Asn Ser Gly Lys	
175	335	340
176	340	345
177	TTG GTC CCT GGT TTT GGA CAT GGA GTT CTG CGA AAG ACT GTA CCA AGA	1164
178	Val Val Pro Gly Phe Gly His Gly Val Leu Arg Lys Thr Val Pro Arg	
179	350	355
180	355	360
181	TAT ACA TGC CAG AGA GAG TTC GCT ATG AAG CAT TTG CCT GAA GAT CCA	1212
182	Tyr Thr Cys Gln Arg Glu Phe Ala Met Lys His Leu Pro Glu Asp Pro	
183	365	370
184	370	375
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186	380	385
187	385	390
188	390	395
189	CTG TTT CAA CTG GTT TCA AAA CTC TAC GAA GTT TTC CTC CTG TTC TTA	1260
190	Leu Phe Gln Leu Val Ser Lys Leu Tyr Glu Val Phe Leu Leu Phe Leu	
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193	405	410
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195	415	420
196	420	425
197	GGT GTG TTG TTG AAC TAT TAT GGT TTA ACT GAA GCA AGA TAT TAT ACG	1356
198	Gly Val Leu Leu Asn Tyr Tyr Gly Leu Thr Glu Ala Arg Tyr Tyr Thr	
199	425	430
200	430	435
201	435	440
202	440	445
203	445	450
204	450	455
205	455	460
	ATG GAG TGG CTT GAG AAC CAG TGC AAG AAA GCA TGAATTGTTT GAAATCTCGC	1452
	Met Glu Trp Leu Glu Asn Gln Cys Lys Lys Ala	
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208 GAGCATAAAA CACAATGTAT AATCTCTATG AATAATTGCT TGACAAAGCA CTCCTTCCTT 1565  
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210 GGGGGACAAG ATAGGTCGGC CCTTCAATGG GTTAACGAAC TTCAGTTCAA ACTTCACTGA 1625  
211  
212 ATTTGTGTGA ATTGTATGGT TTCTCGAGAC TTGTCCTGAA TTTTGAACCTT AGTCTAGTGG 1685  
213  
214 ATTCATTTT CTTCATTCCG AATTCTCAC ACGCTGATCC AGCATGTAAA AATTAATAGG 1745  
215  
216 TCAATGCTAT TAATCGCGTT CTTGGTTGCC ATTAGACTTG TGAATGACTT CCTTGCTGG 1805  
217  
218 AAAGTTAGTA ATCGGCTGAT TCACGCAATA AACTGCAATT GTGTAGTTTC TTAAATTTGC 1865  
219  
220 TAATTCTTAT TTGATGATAT TATGAA 1891  
221  
222  
223 (2) INFORMATION FOR SEQ ID NO:2:  
224  
225 (i) SEQUENCE CHARACTERISTICS:  
226 (A) LENGTH: 471 amino acids  
227 (B) TYPE: amino acid  
228 (D) TOPOLOGY: linear  
229  
230 (ii) MOLECULE TYPE: protein  
231  
232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
233  
234 Met Val Phe Tyr Arg Ser Val Ser Leu Leu Ser Lys Leu Arg Ser Arg  
235 1 5 10 15  
236  
237 Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg Trp Leu Gln Val  
238 20 25 30  
239  
240 Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu Val Gln Glu Leu  
241 35 40 45  
242  
243 Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Ile Lys Ser Asp Met Lys  
244 50 55 60  
245  
246 Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Met Arg  
247 65 70 75 80  
248  
249 Gly Met Thr Gly Leu Leu Trp Lys Pro His Tyr Leu Asp Pro Asp Glu  
250 85 90 95  
251  
252 Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys Gln Lys Val Leu  
253 100 105 110  
254  
255 Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu Gly Leu Leu Trp  
256 115 120 125  
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258 Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asn Ser Ile

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**SEQUENCE VERIFICATION REPORT**  
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